

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:20:40 ; Search time 7.9771 Seconds
(without alignments)
228.975 Million cell updates/sec

Title: US-09-787-082-8

Perfect score: 119

Sequence: 1 GCCSNPVCHELSNLTNG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	85.7	16	2 A59046	alpha-conotoxin MI
2	54	45.4	16	2 A59042	alpha-conotoxin Ep
3	54	45.4	589	2 B38128	epithelin/granulin
4	51	42.9	16	2 A59045	alpha-conotoxin Au
5	50.5	42.4	1101	2 T16840	hypothetical prote
6	50	42.0	16	2 C59045	alpha-conotoxin Au
7	50	42.0	16	2 B54877	alpha-conotoxin Pn
8	49.5	41.6	151	2 T20071	hypothetical prote
9	48.5	40.8	130	2 F82063	hypothetical prote
10	48.5	40.8	644	2 A36325	epidermal growth f
11	48.5	40.8	1210	2 A53183	epidermal growth f
12	48	40.3	160	2 T25185	hypothetical prote
13	48	40.3	593	1 GXHU	granulin precursor
14	47	39.5	18	1 A58589	alpha-conotoxin EI
15	47	39.5	566	2 S19307	carboxylesterase (
16	46.5	39.1	728	2 I50719	C-Delta-1 - chicke
17	46	38.7	54	2 A31436	ovomucoid, third d
18	45.5	38.2	159	2 T33696	hypothetical prote
19	45.5	38.2	601	2 A27020	DiF-induced presta
20	45.5	38.2	1046	2 A26838	prestalk protein p
21	45	37.8	16	2 A54877	alpha-conotoxin P
22	45	37.8	19	2 A44379	alpha-conotoxin SI
23	45	37.8	506	2 S50937	hypothetical prote
24	44.5	37.4	434	2 C27827	S-locus-specific g
25	44	37.0	49	2 I48946	cellular dsintegr
26	44	37.0	318	2 E87929	protein T22H2.6 [1
27	44	37.0	345	2 T25138	hypothetical prote
28	44	37.0	356	2 T40265	hypothetical zinc-
29	44	37.0	358	2 T25137	hypothetical prote

30	44	37.0	423	2 AC3553	4-aminobutyrate tr
31	44	37.0	493	2 T01206	cysteine proteinas
32	44	37.0	527	2 T01019	transport protein
33	44	37.0	689	2 T42760	fibulin, splice fo
34	44	37.0	712	2 T42990	fibulin 1, splice
35	44	37.0	798	2 T22793	hypothetical prote
36	43	36.1	15	2 B59045	alpha-conotoxin Au
37	43	36.1	124	2 AG2339	hypothetical prote
38	43	36.1	186	2 G89614	protein FL5G9.5 [1
39	43	36.1	272	2 T20991	hypothetical prote
40	43	36.1	294	2 T23682	hypothetical prote
41	43	36.1	337	2 T18431	hypothetical prote
42	43	36.1	357	2 S23403	sperm surface prot
43	43	36.1	366	2 C87624	alcohol dehydrogen
44	43	36.1	399	2 T38388	hypothetical wd-40
45	43	36.1	471	2 T41602	hypothetical prote

ALIGNMENTS

RESULT 1

A59046

alpha-conotoxin MII - cone shell (Conus magus)

C;Species: Conus magus (magus cone)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: A59046

R;Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 7522-7528, 1996

A;Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine rec

A;Reference number: A59046; MUID:96205934; PMID:8631783

A;Accession: A59046

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <CAR>

C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;1-16/Product: alpha-conotoxin MII #status experimental <MAT>

F;2-8,3-16/Disulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 85.7%; Score 102; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCSNPVCHELSNLC 16

|||||

Db 1 GCCSNPVCHELSNLC 16

RESULT 2

A59042

alpha-conotoxin Epi - cone shell (Conus episcopatus)

C;Species: Conus episcopatus (bishop's cone)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999

C;Accession: A59042

R;Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett,

J. Biol. Chem. 273, 15667-15674, 1998

A;Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that s

A;Reference number: A59042; MUID:98288307; PMID:9624161

A;Accession: A59042

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <LOO>

C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;1-16/Product: alpha-conotoxin Epi #status experimental <MAT>

F;2-8,3-16/Disulfide bonds: #status experimental

F;15/Binding site: sulfate (Tyr) (covalent) #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 45.4%; Score 54; DB 2; Length 16;

Best Local Similarity 43.8%; Pred. No. 0.7;

```
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCCSNPVCCHLEHSLNC 16
    ||||| |::: |
Db 1 GCCSDPRCMMNPNDYC 16

RESULT 3
B38128
epithelin/granulin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C:Accession: B38128; A36199; B36199; E36698; I53272
R:Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.D.
J. Biol. Chem. 267, 13073-13078, 1992
A:Title: The epithelin precursor encodes two proteins with opposing activities on epithelial cells
A:Reference number: A38128; MUID:92317004; PMID:1618805
A:Accession: B38128
A:Molecule type: mRNA
A:Residues: 1-589 <PLOS>
A:Cross-references: GB:X62322; NID:956108; PIDN:CAA44198.1; PID:956109
R:Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
A:Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth factors
A:Reference number: A36199; MUID:91045907; PMID:2236009
A:Accession: A36199
A:Molecule type: protein
A:Residues: 280-300 <SHO>
A:Accession: B36199
A:Molecule type: protein
A:Residues: 205-226 <SH2>
R:Batemán, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A:Title: Granulins, a novel class of peptide from leukocytes.
A:Reference number: A36698; MUID:91097544; PMID:2268320
A:Accession: E36698
A:Molecule type: protein
A:Residues: 279-307 'SB', 310-324 'T', 326, 'X', 328, 'Q' <BAT>
R:Bhandari, V.; Gialdini, A.; Bateman, A.
Endocrinology 133, 2682-2689, 1993
A:Title: The complementary deoxyribonucleic acid sequence, tissue distribution, and cell expression of the human granulins gene
A:Reference number: I53272; MUID:94062640; PMID:8243292
A:Accession: I53272
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-200, 'S', 203-388, 'W', 390-589 <RES>
A:Cross-references: GB:M97750; NID:9204223; PIDN:AAAL6903.1; PID:g204224
C:Superfamily: granulin

Query Match 45.4%; Score 54; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 GCCSNP--VCHLEHSLNCTNG 19
    ||| | | | | | | |
Db 385 GCCPIPEAVCCLDHQHCCPQG 405

RESULT 4
A59045
alpha-conotoxin Au1C - cone shell (Conus aulicus)
C:Species: Conus aulicus (court cone)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: A59045
R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.
Neurosci. 18, 8571-8579, 1998
A:Title: Alpha-conotoxin Au1B selectively blocks alpha3beta4 nicotinic acetylcholine receptors
A:Reference number: A59045; MUID:99003392; PMID:9786965
A:Accession: A59045
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <LUO>
C:Superfamily: alpha-conotoxin

Query Match 45.4%; Score 54; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
```

```
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuromuscular transmission; alpha-conotoxin Au1A #status experimental <MAT>
F:1-16/Product: alpha-conotoxin Au1A #status experimental
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.9%; Score 51; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCSNPVCCHLEHSLNC 16
    ||||| | | | |
Db 1 GCCSYPPCFATNSDYC 16

RESULT 5
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Geisler, C.
Submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E10.4
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3

Query Match 42.4%; Score 50.5; DB 2; Length 1101;
Best Local Similarity 33.3%; Pred. No. 47;
Matches 10; Conservative 3; Mismatches 6; Indels 11; Gaps 1;

QY 1 GCC-----SNPVCCHLEHSLNCTNG 19
    ||| | | | | | | |
Db 840 GCCLLSMEPVCPTSRNAVQCSPNNVCPFG 869

RESULT 6
CS9045
alpha-conotoxin Au1C - cone shell (Conus aulicus)
C:Species: Conus aulicus (court cone)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: CS9045
R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.
Neurosci. 18, 8571-8579, 1998
A:Title: Alpha-conotoxin Au1B selectively blocks alpha3beta4 nicotinic acetylcholine receptors
A:Reference number: A59045; MUID:99003392; PMID:9786965
A:Accession: CS9045
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <LUO>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuromuscular transmission; alpha-conotoxin Au1C #status experimental <MAT>
F:1-16/Product: alpha-conotoxin Au1B #status experimental
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.0%; Score 50; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCCSNPVCCHLEHSLNC 16
    ||||| | | | |
Db 1 GCCSYPPCFATNSGYC 16

RESULT 7
```

B54877
alpha-conotoxin Pn1B - cone shell (Conus pennaceus)
C:Species: Conus pennaceus
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
C:Accession: B54877
R:Painzliber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk
Biochemistry 33, 9523-9529, 1994
A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece
A:Reference number: A54877; MUID:94347719; PMID:8068627
A:Accession: B54877
A:Molecule type: protein
A:Residues: 1-16 <FAI>
A:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.0%; Score 50; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCSNPVCCHLEHSLNLC 16
||||| : : : :
DB 1 GCCSUPPCALSNPDYC 16

RESULT 8
T20071
hypothetical protein C49F5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20071
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19219
A:Accession: T20071
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-151 <WIL>
A:Cross-references: EMBL:Z81485; PIDN:CAB03976.1; GSPDB:GN00028; CESP:C49F5.5
A:Experimental source: clone C49F5
C:Genetics:
A:Gene: CESP:C49F5.5
A:Map position: X
A:Introns: 36/2; 72/3; 115/1

Query Match 41.6%; Score 49.5; DB 2; Length 151;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

QY 3 CSNPVC----HLEHSLNCTNG 19
| | | | | : : : :
DB 89 CDLPSCGLFKYTLSHLNMCTNG 110

RESULT 9
F82063
hypothetical protein VC2540 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82063
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82063
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <HEI>
A:Cross-references: GB:AE004323; GB:AE003852; NID:g9657119; PIDN:AAF95681.1; GSPDB:GN0001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2540
A:Map position: 1

Query Match 40.8%; Score 48.5; DB 2; Length 130;
Best Local Similarity 61.1%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 GCCSNPVCCHLEHSLNCTN 18
|| ||| : : : :
DB 95 GCVSNPWCCL-CSVCCTN 111

RESULT 10
A36325
epidermal growth factor receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
C:Accession: A36325
R:Petch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.S.
Mol. Cell. Biol. 10, 2973-2982, 1990
A:Title: A truncated, secreted form of the epidermal growth factor receptor is encode
A:Reference number: A36325; MUID:90258888; PMID:2342466
A:Accession: A36325
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-644 <PET>
A:Cross-references: GB:M37394
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: alternative splicing; ATP; growth factor receptor

Query Match 40.8%; Score 48.5; DB 2; Length 644;
Best Local Similarity 62.5%; Pred. No. 57;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 SNPVCCHLEHSLNCTNG 19
: ||||| : : : :
DB 613 ANNVCHLCHAN-CTYG 627

RESULT 11
A53183
epidermal growth factor receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C:Accession: A53183; A43818; S24942; A28941; S45325; I49643
R:Luetkeke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A
Genes Dev. 8, 399-413, 1994
A:Title: The mouse waved-2 phenotype results from a point mutation in the EGF recept
A:Reference number: A53183; MUID:94170986; PMID:8125255
A:Accession: A53183
A:Molecule type: mRNA
A:Residues: 1-1210 <LUE>
A:Cross-references: GB:U03425
R:Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.
Oncogene 6, 673-676, 1991
A:Title: Comparison of EGF receptor sequences as a guide to study the ligand binding
A:Reference number: A43818; MUID:91232866; PMID:2030916
A:Accession: A43818
A:Molecule type: mRNA
A:Residues: 1-714 <AVI>
A:Cross-references: GB:X59698
R:Eisinger, D.P.; Serrero, G.
submitted to the EMBL Data Library, June 1992
A:Reference number: S24942
A:Accession: S24942
A:Molecule type: mRNA
A:Residues: 969-971, 'K', 973-1115, 'D' <EIS>
A:Cross-references: EMBL:Z12608
R:Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A:Title: Epidermal growth factor receptor threonine and serine residues phosphorylate

A:Reference number: A28941; MUID:88330814; PMID:3138233
A:Accession: A28941
A:Molecule type: protein
A:Residues: 689-694, 'X', 706-707, 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1009,
R: Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
Submitted to the EMBL Data Library, April 1994
A:Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
A:Reference number: S45325
A:Accession: S45325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-971, 'K', 973-1210 <VER>
A:Cross-references: EMBL:X78987; NID:9488830; PIDN:CAA55587.1; PID:9488831
R: Paria, B.C.; Das, S.K.; Andrews, G.K.; Dev, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A:Title: Expression of the epidermal growth factor receptor gene is regulated in mouse b
A:Reference number: 149643; MUID:93126380; PMID:7678348
A:Accession: 149643
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 12-20, 22-132 <RES>
A:Cross-references: GB:L06864; NID:9193001; PIDN:AAA53029.1; PID:g567201
C:Genetics:
A:Gene: EGFR
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphop
F:1-24/Domain: signal sequence #status predicted <SIG>
F:648-670/Domain: transmembrane #status predicted <TM>
F:712-977/Domain: protein kinase homology <KIN>
F:720-728/Region: protein kinase ATP-binding motif
F:680, 695/Binding site: phosphate (Thr) (covalent) #status experimental
F:697, 1070, 1071/Binding site: phosphate (Ser) (covalent) #status experimental
F:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F:1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 40.8%; Score 48.5; DB 2; Length 1210;
Best Local Similarity 62.5%; Pred. NO. 92;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 4 SNPVCHLSNCTNG 19
: | | | | | | | | | |
Db 613 ANNVCHLAN-CTYG 627

RESULT 12
T25185
hypothetical protein T23F6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25185
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19992
A:Accession: T25185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-160 <WIL>
A:Cross-references: EMBL:Z83127; PIDN:CAB05630.1; GSPDB:GN00022; CESP:T23F6.1
A:Experimental source: clone T23F6
C:Genetics:
A:Gene: CESP:T23F6.1
A:Map position: 4
A:Introns: 76/3; 124/3

Query Match 40.3%; Score 48; DB 2; Length 160;
Best Local Similarity 52.9%; Pred. No. 24;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

OY 3 CSNPVCHLSNCTNG 19
: | | | | | | | | | |
Db 113 CCQPCV-CTNACTNG 125

RESULT 13

GIHU
granulin precursor [validated] - human
N:Alternate names: epithelin
N:Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F; g
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C:Accession: JCI284; A38128; A36698; B36698; C36698; D36698; A56873
R:Bhandari, V.; Bateman, A.
Biochem. Biophys. Res. Commun. 188, 57-63, 1992
A:Title: Structure and chromosomal location of the human granulin gene.
A:Reference number: JCI284; MUID:93038704; PMID:1417868
A:Accession: JCI284
A:Molecule type: DNA
A:Residues: 1-593 <SHA>
R: Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, J. Biol. Chem. 267, 13073-13078, 1992
A:Title: The epithelin precursor encodes two proteins with opposing activities on epi
A:Reference number: A38128; MUID:92317004; PMID:1618805
A:Accession: A38128
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-593 <PILO>
A:Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193
R:Bhandari, V.; Pallfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A:Title: Isolation and sequence of the granulin precursor cDNA from human bone marrow
A:Reference number: A38118; MUID:92179253; PMID:1542665
A:Accession: A38118
A:Molecule type: mRNA
A:Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'Q', 461-546, 'A', 548-566, 'R', 568
A:Cross-references: GB:M75161; NID:g183612; PIDN:AAA58617.1; PID:g183613
A:Note: this sequence has been revised in reference JCI284
R: Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A:Title: Granulins, a novel class of peptide from leukocytes.
A:Reference number: A36698; MUID:91097544; PMID:2268320
A:Accession: A36698
A:Molecule type: protein
A:Residues: 281-336 <BAT>
A:Note: this protein was purified and characterized as granulin A
A:Accession: B36698
A:Molecule type: protein
A:Residues: 206-218, 'H', 220-233 <BA2>
A:Note: this protein was purified and characterized as granulin B
A:Accession: C36698
A:Molecule type: protein
A:Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>
A:Note: this protein was purified and characterized as granulin C
A:Accession: D36698
A:Molecule type: protein
A:Residues: 442-446, 'XDTSS', 456-458, 'DG', <BA4>
R: Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A:Title: Characterisation of UGP and its relationship with beta-core fragment.
A:Reference number: A56873; MUID:93229246; PMID:8471426
A:Accession: A56873
A:Molecule type: protein
A:Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBIP:129524)
C:Genetics:
A:Gene: GDB:GRN
A:Cross-references: GDB:136006; OMIM:138945
A:Map position: 17pter-17qter
A:Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3
C:Superfamily: granulin
C:Keywords: glycoprotein; tandem repeat
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-593/Product: granulin #status predicted <MAR>
F:18-593/Product: progranulin #status predicted <PRO>
F:18-44/Product: paraganulin #status experimental <PGR>

F:58-113/Product: granulin G #status predicted <GRG>
F:123-179/Product: granulin F #status predicted <GRF>
F:206-261/Product: granulin B #status experimental <GRB>
F:281-336/Product: granulin A #status experimental <GRA>
F:364-417/Product: granulin C #status experimental <GRC>
F:442-496/Product: granulin D #status predicted <GRD>
F:518-573/Product: granulin E #status predicted <GRE>
F:368/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 40.3%; Score 48; DB 1; Length 593;
Best Local Similarity 42.9%; Pred. No. 63;
Matches 9; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 1 GCCSNP-VCHLEHSLNCTNG 19
||| | || : | : | : |
Db 387 GCCPIPEAVCCSDHQHCCPQG 407

RESULT 14
A35889
alpha-conotoxin EI - cone shell (Conus ermineus)
C:Species: Conus ermineus (ermine cone)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A58589
R:Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;
Biochemistry 34, 14519-14526, 1995
A:Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with novel
A:Reference number: A58589; MUID:96062516; PMID:7578057
A:Accession: A58589
A:Molecule type: protein
A:Residues: 1-18 <MAR>
A:Note: sequence confirmed by chemical synthesis
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
F:4-10,5-18/Disulfide bonds: #status experimental
F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 39.5%; Score 47; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 6.2;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCSNPVCHLEHSLNLC 16
|| : | : : : |
Db 4 CCYHPTCNMNPQIC 18

RESULT 15
S19307
carboxylesterase (EC 3.1.1.1) precursor - pig
N:Alternate names: proline-beta-naphthylamidase
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999
C:Accession: S19307; S23607
R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahashi
FEBS Lett. 293, 37-41, 1991
A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-n
A:Reference number: S19307; MUID:92070571; PMID:1959668
A:Accession: S19307
A:Molecule type: mRNA
A:Residues: 1-566 <MAT1>
A:Cross-references: EMBL:X63323; NID:g1930; PIDN:CAA44929.1; PID:g1931
A:Accession: S23607
A:Molecule type: protein
A:Residues: 19-40 <MAT2>
A:Note: 28-Lys and 33-Leu were also found
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-566/Product: carboxylesterase #status experimental <MAT>
F:51-552/Domain: cholinesterase homology <CHE>
F:80/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:222,467/Active site: Ser, His #status predicted

Query Match 39.5%; Score 47; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 CCSNPVCHLEHSLNCTNG 19
|| : | : | : | : |
Db 88 CCODPVVEQMTSDLFTNG 105

Search completed: March 17, 2003, 07:27:28
Job time : 9.9771 secs

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